



SEQUENCE LISTING

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Dropulic, Boro
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<120> IMPROVED CONDITIONALLY REPLICATING VECTORS
FOR INHIBITING VIRAL INFECTIONS

<130> 39727-20007.00

<140> US 09/819,401

<141> 2001-03-27

<160> 18

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide encoded wild-type HIV US sequence

<400> 1

gtgtgcccgt ctgttggtg actctggtaa ctagagatc

39

<210> 2

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Vector sequence

<400> 2

gtgtgcccac ctgttggtg actctggcag ctagagaac

39

<210> 3

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence encoded ribozyme

<400> 3

cacacaacac tgatgaggcc gaaaggccga aacgggcaca

40

<210> 4
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Sequence encoded ribozyme

 <400> 4
 atctctagtc tgatgaggcc gaaaggccga aaccagagtc 40

 <210> 5
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Vector sequence

 <400> 5
 gtgtgcccgc ctgttggtgtg actctggtaa ctagagatc 39

 <210> 6
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Vector sequence

 <400> 6
 gtgtgcccgt ctgttggtgtg actctggcaa ctagagatc 39

 <210> 7
 <211> 15
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Consensus splice donor

 <221> misc_feature
 <222> (1)...(15)
 <223> n = A,T,C or G

 <400> 7
 nnnnaggtaa gttnnn 15

 <210> 8
 <211> 15
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Beta-globin splice donor

 <221> misc_feature

<222> (1)...(15)
 <223> n = A,T,C or G

 <400> 8
 ngggcaggta agtat 15

 <210> 9
 <211> 15
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> HIV major splice donor

 <221> misc_feature
 <222> (1)...(15)
 <223> n = A,T,C or G

 <400> 9
 nngactggtg agtan 15

 <210> 10
 <211> 15
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> HIV-1 env splice donor

 <400> 10
 aaagcagtaa gtagt 15

 <210> 11
 <211> 15
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> HIV-2 env splice donor

 <400> 11
 agacaagtga gtaag 15

 <210> 12
 <211> 15
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> HIV-2 major splice donor

 <221> misc_feature
 <222> (1)...(15)
 <223> n = A,T,C or G

 <400> 12
 nngaaggtaa gtgcn 15

<210> 13
 <211> 112
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Double-stranded oligonucleotide

 <400> 13
 aagcttgccct tgagtgtca aagtagtgtg tgcccacctg ttgtgtgact ctggcagcta 60
 gagatccac agaccctttt agtcagtgtg gaaaatctct agcagtggcg cc 112

 <210> 14
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide with mutant nucleotides

 <221> misc_feature
 <222> (1)...(39)
 <223> n = A,T,C or G

 <400> 14
 gtgtgcccnn ctgttgtgtg actctggan ctagaganc 39

 <210> 15
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Mutated oligonucleotide

 <400> 15
 gtgtgcccct ctgttgtgtg actctggtaa ctagagatc 39

 <210> 16
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Mutated oligonucleotide

 <400> 16
 gtgtgcccgt ctgttgtgtg actctggtag ctagagatc 39

 <210> 17
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Analog splice donor

<221> misc_feature
 <222> (1)...(16)
 <223> n = A,T,C or G

<400> 17
 cttcaggggtg agttnn

16

<210> 18
 <211> 1185
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of a chimeric HIV CTL epitope

<400> 18
 Met Lys Ile Arg Leu Arg Pro Gly Gly Asn Lys Lys Tyr Lys Leu Lys
 1 5 10 15
 His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Gly Ser Glu Glu
 20 25 30
 Leu Arg Ser Leu Tyr Asn Thr Val Ala Val Leu Tyr Cys Val His Gln
 35 40 45
 Lys Ile Glu Val Lys Asp Thr Lys Glu Ala Leu Asp Thr Glu Asn Arg
 50 55 60
 Asn Gln Glu Ser Gln Asn Tyr Pro Ile Val Gln Asn Leu Gly Gln Met
 65 70 75 80
 Val His Gln Ala Leu Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val
 85 90 95
 Ile Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala
 100 105 110
 Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr
 115 120 125
 Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Ala Thr Ile Asn
 130 135 140
 Glu Glu Ala Ala Glu Trp Asp Arg Leu His Pro Val His Ala Gly Pro
 145 150 155 160
 Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Thr Ser Thr Leu Gln
 165 170 175
 Glu Gln Ile Ala Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly Glu
 180 185 190
 Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg Met
 195 200 205
 Tyr Ser Pro Val Ser Ile Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys
 210 215 220
 Thr Leu Arg Ala Glu Gln Ala Thr Gln Glu Val Lys Asn Trp Met Thr
 225 230 235 240
 Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu
 245 250 255
 Lys Ala Leu Leu Glu Asp Met Met Thr Ala Cys Gln Gly Val Gly Gly
 260 265 270
 Pro Gly His Lys Ala Arg Leu Val Gln Glu Gly His Gln Met Lys Asp
 275 280 285
 Cys Thr Glu Arg Gln Ala Asn Phe Gly Asn Phe Pro Gln Ser Arg Leu
 290 295 300
 Glu Pro Thr Ala Pro Pro Glu Ile Thr Leu Trp Gln Arg Pro Leu Val
 305 310 315 320

Asp	Thr	Val	Leu	Glu	Asp	Met	Asn	Leu	Val	Leu	Val	Gly	Pro	Thr	Pro	
				325					330						335	
Val	Asn	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Gly	Pro	Lys	
			340					345					350			
Val	Lys	Gln	Trp	Pro	Leu	Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Met	Glu	
		355					360					365				
Lys	Glu	Gly	Lys	Ile	Ser	Lys	Ile	Gly	Pro	Thr	Val	Leu	Asp	Val	Gly	
	370					375					380					
Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Glu	Asp	Phe	Arg	Lys	Tyr	Thr	
385					390					395					400	
Ala	Phe	Thr	Ile	Pro	Ser	Ile	Trp	Lys	Gly	Ser	Pro	Ala	Ile	Phe	Gln	
			405						410					415		
Ser	Ser	Met	Thr	Lys	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	
			420					425					430			
Asp	Leu	Tyr	Val	Asp	Leu	Glu	Glu	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	
	435						440					445				
Glu	Leu	Arg	Gln	His	Leu	Leu	Arg	Trp	Gly	Phe	Thr	Thr	Pro	Asp	Lys	
	450					455					460					
Lys	Pro	Ile	Lys	Leu	Pro	Glu	Lys	Glu	Ser	Trp	Leu	Val	Gly	Lys	Leu	
465					470				475						480	
Asn	Trp	Ala	Ser	Gln	Ile	Tyr	Ala	Gly	Ile	Lys	Val	Lys	Gln	Leu	Ile	
			485						490					495		
Pro	Ile	Thr	Glu	Glu	Ala	Glu	Leu	Glu	Ile	Leu	Lys	Glu	Pro	Val	His	
			500					505					510			
Gly	Val	Tyr	Gln	Ile	Tyr	Gln	Glu	Pro	Phe	Lys	Asn	Leu	Lys	Thr	Gly	
	515						520					525				
Asp	Val	Lys	Gln	Leu	Thr	Glu	Ala	Val	Lys	Ile	Thr	Thr	Glu	Ser	Ile	
	530					535					540					
Val	Ile	Trp	Pro	Ile	Gln	Lys	Glu	Thr	Trp	Glu	Thr	Trp	Trp	Thr	Glu	
545					550					555					560	
Tyr	Trp	Pro	Leu	Val	Lys	Leu	Trp	Tyr	Gln	Leu	Glu	Pro	Ile	Val	Gly	
			565						570					575		
Ala	Glu	Thr	Phe	Tyr	Val	Asp	Gly	Ala	Ala	Asn	Lys	Ala	Leu	Gln	Asp	
			580					585					590			
Ser	Gly	Leu	Glu	Val	Asn	Ile	Val	Thr	Asp	Ser	Gln	Tyr	Ala	Leu	Gly	
	595						600					605				
Ile	Glu	Ser	Glu	Leu	Val	Ser	Gln	Ile	Ile	Glu	Gln	Leu	Leu	Ala	Trp	
	610					615					620					
Val	Pro	Ala	His	Lys	Gly	Tyr	Glu	Glu	Ala	Glu	Val	Ile	Glu	Thr	Ala	
625					630					635					640	
Tyr	Phe	Ile	Leu	Lys	Leu	Leu	Leu	Trp	Lys	Gly	Glu	Gly	Ala	Val	Ile	
			645						650					655		
Ser	Gly	Trp	Ile	Leu	Asn	Thr	Tyr	Arg	Val	Lys	Gly	Ile	Arg	Lys	Asn	
		660						665					670			
Tyr	Ala	Glu	Asn	Leu	Trp	Val	Thr	Val	Tyr	Tyr	Gly	Val	Pro	Val	Trp	
	675						680					685				
Lys	Glu	Ala	Thr	Thr	Thr	Leu	Phe	Cys	Ala	Ser	Asp	Ala	Lys	Ala	Tyr	
	690					695					700					
Asp	Pro	Asn	Pro	Gln	Glu	Val	Val	Leu	His	Glu	Asp	Ile	Ile	Ser	Leu	
705					710					715					720	
Trp	Asp	Gln	Ser	Leu	Lys	Lys	Leu	Thr	Pro	Leu	Cys	Val	Thr	Leu	Asn	
			725						730					735		
Cys	Ser	Phe	Asn	Val	Thr	Thr	Leu	Ile	Asn	Thr	Ser	Tyr	Thr	Leu	Ile	
		740					745						750			
Asn	Cys	Lys	Ser	Ser	Thr	Ile	Thr	Gln	Ala	Cys	Pro	Lys	Cys	Lys	Asn	
	755						760					765				
Val	Ser	Thr	Val	Gln	Cys	Arg	Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	

770		775		780
Asn Gly Ser Leu Ala Glu Glu Asp Ile Val Ser Ile Glu Ile Asn Cys				
785		790		795
Thr Arg Pro Asn Asn Asn Thr Arg Lys Lys Ile Thr Leu Gly Pro Gly				800
	805		810	815
Arg Val Leu Tyr Thr Thr Gly Glu Asn Asn Thr Leu Lys Gln Ile Val				
	820		825	830
Glu Lys Leu Arg Glu Ile Lys Gln Phe Lys Pro Glu Ile Val Met His				
	835		840	845
Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu				
	850		855	860
Phe Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Arg Trp Gln Glu Val				
	865		870	875
Gly Lys Ala Met Tyr Ala Pro Pro Ile Glu Gly Gln Ile Arg Cys Leu				
	885		890	895
Ser Asn Ile Thr Gly Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr				
	900		905	910
Lys Ala Lys Arg Arg Val Val Gln Arg Arg Ala Ile Glu Ala Gln Gln				
	915		920	925
His Leu Gly Ile Lys Gln Leu Gln Ala Arg Val Leu Ala Val Glu Arg				
	930		935	940
Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Thr Thr Val Pro Trp Asn				
	945		950	955
Ala Ser Trp Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Val Leu				
	965		970	975
Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln				
	980		985	990
Thr His Arg Leu Val Asp Gly Phe Leu Thr Leu Leu Tyr His Arg Leu				
	995		1000	1005
Ile Asp Leu Leu Leu Ile Ala Lys Arg Gly Arg Arg Gly Trp Ala Ala				
	1010		1015	1020
Leu Lys Tyr Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Asp Arg Val				
	1025		1030	1035
Ile Glu Ile Val Gln Arg Thr Cys Arg Ala Ile Leu His Ile Pro Arg				
	1045		1050	1055
Arg Ile Arg Gln Gly Leu Glu Arg Ala Leu Leu Trp Pro Ala Ile Arg				
	1060		1065	1070
Glu Arg Met Val Gly Phe Pro Val Arg Pro Gln Val Pro Leu Arg Pro				
	1075		1080	1085
Met Thr Tyr Lys Ala Ala His Asp Leu Ser His Phe Leu Lys Glu Lys				
	1090		1095	1100
Gly Gly Leu Glu Gly Leu Ile Tyr Ser Gln Lys Arg Gln Asp Ile Leu				
	1105		1110	1115
Asp Leu Trp Val Tyr His Thr Gln Gly Phe Phe Pro Asp Trp Gln Asn				
	1125		1130	1135
Tyr Thr Pro Gly Pro Gly Thr Arg Tyr Pro Leu Cys Phe Gly Trp Cys				
	1140		1145	1150
Phe Lys Leu Val Pro Val Val Leu Met Trp Lys Phe Asp Ser Lys Leu				
	1155		1160	1165
Ala Phe His His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asp				
	1170		1175	1180
Cys				
1185				